AMENDMENTS TO THE CLAIMS;

This listing of claims will replace all prior versions and listing of the claims in the application:

LISTING OF THE CLAIMS:

Claim 1. (Currently amended) A method for preparing a variant polynucleotide having a nucleotide sequence not identical to either of at least two parent polynucleotides comprising;

preparing at least one heteroduplex between said at least two parent polynucleotides wherein said heteroduplex has at least two mismatch sites separated by at least one complementary nucleotide base pair,

cleaving at least one polynucleotide strand in said heteroduplex ~~at~~ within six nucleotides 3' of a mismatch site with an effective amount of mismatch-directed strand cleavage activity to form a cleavage site,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site,

wherein at least one ~~of said~~ polynucleotide strand[s] is formed that has a nucleotide sequence not identical to either of said at least two parent polynucleotides or the complementary sequences of said at least two parent polynucleotides.

Claim 2. (Original) The method of claim 1 wherein the polynucleotides forming a heteroduplex are circular.

Claim 3. (Canceled)

Claim 4. (Previously presented) The method of claim 1 wherein said at least one heteroduplex contains a gene.

Claim 5. (Previously presented) The method of claim 4 wherein said at least one heteroduplex is a genome.

Claim 6. (Canceled)

Claim 7. (Currently amended) A method for preparing a variant polynucleotide having a nucleotide sequence not identical to any of at least three parent polynucleotides comprising;

preparing at least two different heteroduplexes among said at least three parent polynucleotides wherein each of said at least two different heteroduplexes has at least two mismatch sites separated by at least one complementary nucleotide base pair,

cleaving at least one polynucleotide strand in said heteroduplexes ~~at~~ within six nucleotides 3' of a mismatch site with an effective amount of mismatch-directed strand cleavage activity to form a cleavage site,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site,

wherein at least one ~~of said~~ polynucleotide strand[s] is formed that has a nucleotide sequence not identical to any of said at least three parent polynucleotides or the complementary sequences of said at least three parent polynucleotides.

Claim 8. (Original) The method of claim 1 wherein a plurality of variant polynucleotides are formed.

Claim 9. (Currently amended) A method for obtaining ~~a~~ polynucleotide sequence variants encoding a desired functional property comprising;

preparing at least one heteroduplex from at least two parent polynucleotides;

cleaving at least one polynucleotide strand in said heteroduplex ~~at~~ within six nucleotides 3' of a mismatch site with an effective amount of mismatch-directed strand cleavage activity to form a cleavage site, replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site, wherein a plurality of variant polynucleotide strands are formed which have nucleotide sequences not identical to either of said at least two parent polynucleotides or the complementary sequences of said at least two parent polynucleotides to form a population of variants, and

screening or selecting ~~a~~ said population of variants for the desired functional property.

Claim 10. (Currently amended) The method of claim 9 further comprising;

forming a second heteroduplex containing at least one variant polynucleotide strand,

cleaving at least one polynucleotide strand in said second heteroduplex ~~at~~ within six nucleotides 3' of a mismatch site to form a cleavage site,

replacing at least one nucleotide on at least one polynucleotide strand at or near the cleavage site, wherein a plurality of variant polynucleotide strands are formed which have nucleotide sequences not identical to either parent polynucleotide~~s~~ or the complementary sequences of either parent polynucleotide present in said second heteroduplex to form a population of variants, and

screening or selecting said population of variants for the desired functional property.

Claim 11. (Original) The method of claim 9 further comprising converting said variant polynucleotide to RNA before said screening or selecting.

Claim 12. (Original) The method of claim 9 further comprising translating said variant polynucleotide or an RNA transcribed therefrom to produce a polypeptide and wherein said screening or selecting is performed on said polypeptide.

Claims 13-41 (Canceled)

Claim 42. (Currently amended) An *in vitro* method of making a population of sequence variants from a heteroduplex polynucleotide sequence wherein said heteroduplex polynucleotide sequence has at least two non-complementary nucleotide base pairs separated by complementary nucleotide base pairs comprising;

~~mixing~~ exposing copies of the heteroduplex polynucleotide sequence ~~with~~ to an effective amount of mismatch-directed strand cleavage activity wherein said activity does not utilize the MutS/L/H enzyme system, proofreading activity, and ligase activity; and allowing sufficient time for a number of non-complementary nucleotide base pairs to be converted to complementary base pairs, wherein a diverse population of polynucleotide sequences results, wherein at least one polynucleotide sequence in said diverse population is not identical to said heteroduplex polynucleotide sequence or the complementary sequence of said heteroduplex polynucleotide.

Claim 43. (Currently amended) An *in vitro* method of obtaining a polynucleotide sequence encoding a desired functional property comprising;

preparing at least one heteroduplex polynucleotide sequence wherein said heteroduplex has at least two mismatch sites separated by at least one complementary nucleotide base pair;

~~mixing~~ exposing copies of the heteroduplex polynucleotide sequence ~~with~~ to an effective amount of mismatch-directed strand cleavage activity wherein said activity does not utilize the MutS/L/H enzyme system, proofreading activity, and ligase activity;

allowing sufficient time for the percentage of complementarity between strands of the heteroduplex polynucleotide sequence to increase, wherein a diverse population of polynucleotide sequences results, wherein at least one polynucleotide sequence in said diverse population is not identical to said heteroduplex polynucleotide sequence or the complementary sequence of said heteroduplex polynucleotide, and

screening or selecting said population of variants for said desired functional property.